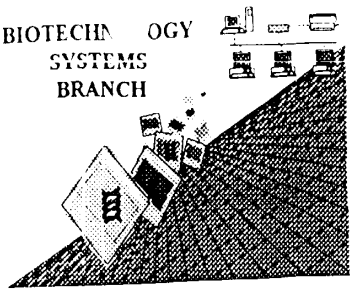

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/872,185

Source: OIPE

Date Processed by STIC: 6-20-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: [illegible]

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10 ✓	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/872,185

DATE: 06/20/2001
TIME: 12:23:27

Input Set : A:\64080.txt
Output Set: N:\CRF3\06202001\I872185.raw

<110> APPLICANT: Stern, David
Herold, Kevan
Yan, Shi Du
Schmidt, Ann Marie
Lamster, Ira
<120> TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
<130> FILE REFERENCE: 0575/64080
C--> <140> CURRENT APPLICATION NUMBER: US/09/872,185
<141> CURRENT FILING DATE: 2001-06-01
<160> NUMBER OF SEQ ID NOS: 16
<170> SOFTWARE: PatentIn version 3.0
<210> SEQ ID NO: 1
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Human
<400> SEQUENCE: 1

```
Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys
1               5                  10                  15
Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn
            20                  25                  30
Thr Gly Arg Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly
        35                  40                  45
Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu
    50                  55                  60
Pro Ala Val Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met
65                  70                  75                  80
Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr
                85                  90                  95
Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr
            100                 105                 110
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<210> SEQ ID NO: 2
<211> LENGTH: 332
<212> TYPE: PRT
<213> ORGANISM: Human
<400> SEQUENCE: 2

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Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys
1               5                  10                  15
Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn
            20                  25                  30
Thr Gly Arg Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly
        35                  40                  45
Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu
    50                  55                  60
Pro Ala Val Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met
65                  70                  75                  80
Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr
                85                  90                  95
```

RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: **US/09/872,185** TIME: 12:23:27

Input Set : **A:\64080.txt**
Output Set: **N:\CRF3\06202001\I872185.raw**

```
73 Gln Ile Pro Gly Ly  Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr
74             100                 105                 110
76 Ala Gly Val Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr
77         115                 120                 125
79 Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro
80     130                 135                 140
82 Asn Glu Lys Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu
83 145                 150                 155                 160
85 Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg
86                 165                 170                 175
88 Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu
89             180                 185                 190
91 Pro Arg His Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp
92         195                 200                 205
94 Glu Pro Val Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly
95     210                 215                 220
97 Gly Ala Val Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro
98 225                 230                 235                 240
100 Ala Gln Pro Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu
101                 245                 250                 255
103 Pro Leu Pro Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln
104             260                 265                 270
106 Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro
107         275                 280                 285
109 Gln Glu Ser Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu
110     290                 295                 300
112 Gly Pro Thr Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala
113 305                 310                 315                 320
115 Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly Thr Ala
116                 325                 330
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 30
120 <212> TYPE: PRT
121 <213> ORGANISM: Peptide
123 <400> SEQUENCE: 3
125 Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys
126 1                 5                  10                  15
128 Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys
129             20                  25                  30
131 <210> SEQ ID NO: 4
132 <211> LENGTH: 30
133 <212> TYPE: PRT
134 <213> ORGANISM: Peptide
136 <400> SEQUENCE: 4
138 Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Ser Cys
139 1                 5                  10                  15
141 Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln Leu Glu Trp Lys
142             20                  25                  30
144 <210> SEQ ID NO: 5
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RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: US/09/872,185 TIME: 12:23:27

Input Set : A:\64080.txt
Output Set: N:\CRF3\06202001\I872185.raw

145 <211> LENGTH: 30
146 <212> TYPE: PRT
147 <213> ORGANISM: Peptide
149 <400> SEQUENCE: 5
151 Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Met Leu Ser Cys
152 1 5 10 15
154 Lys Ala Ala Pro Lys Lys Pro Thr Gln Lys Leu Glu Trp Lys
155 20 25 30
157 <210> SEQ ID NO: 6
158 <211> LENGTH: 30
159 <212> TYPE: PRT
160 <213> ORGANISM: Peptide
162 <400> SEQUENCE: 6
164 Asp Gln Asn Ile Thr Ala Arg Ile Gly Lys Pro Leu Val Leu Asn Cys
165 1 5 10 15
167 Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln Leu Glu Trp Lys
168 20 25 30
170 <210> SEQ ID NO: 7
171 <211> LENGTH: 30
172 <212> TYPE: PRT
173 <213> ORGANISM: Peptide
175 <400> SEQUENCE: 7
177 Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys
178 1 5 10 15
180 Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys
181 20 25 30
183 <210> SEQ ID NO: 8
184 <211> LENGTH: 10
185 <212> TYPE: PRT
186 <213> ORGANISM: Peptide
188 <400> SEQUENCE: 8
190 Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
191 1 5 10
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 50
195 <212> TYPE: PRT
196 <213> ORGANISM: Bovine
198 <220> FEATURE:
199 <221> NAME/KEY: UNSURE
200 <222> LOCATION: (47)..(47)
201 <223> OTHER INFORMATION: Where Xaa unsure
204 <400> SEQUENCE: 9
206 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln
207 1 5 10 15
209 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu
210 20 25 30
W--> 212 Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys
213 35 40 45
215 Asp Gln

RAW SEQUENCE LISTING DATE: 06/20/2001
PATENT APPLICATION: **US/09/872,185** TIME: 12:23:27

Input Set : **A:\64080.txt**
Output Set: **N:\CRF3\06202001\I872185.raw**

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216      50
218 <210> SEQ ID NO: 10
219 <211> LENGTH: 18
220 <212> TYPE: PRT
221 <213> ORGANISM: Bovine
223 <400> SEQUENCE: 10
225 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
226 1               5                  10                  15
228 Leu Lys
231 <210> SEQ ID NO: 11
232 <211> LENGTH: 90
233 <212> TYPE: PRT
234 <213> ORGANISM: Bovine
236 <400> SEQUENCE: 11
238 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
239 1               5                  10                  15
241 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
242             20                  25                  30
244 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
245         35                  40                  45
247 Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
248     50                  55                  60
250 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
251 65                  70                  75                  80
253 Leu Lys Thr Ala His Ile Asp Ile His Lys
254                 85                  90
256 <210> SEQ ID NO: 12
257 <211> LENGTH: 90
258 <212> TYPE: PRT
259 <213> ORGANISM: Bovine
261 <400> SEQUENCE: 12
263 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
264 1               5                  10                  15
266 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
267             20                  25                  30
269 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
270         35                  40                  45
272 Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
273     50                  55                  60
275 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
276 65                  70                  75                  80
278 Leu Lys Thr Ala His Ile Asp Ile His Lys
279                 85                  90
281 <210> SEQ ID NO: 13
282 <211> LENGTH: 21
283 <212> TYPE: DNA
284 <213> ORGANISM: Sense Primer
286 <400> SEQUENCE: 13
287 gtaagcgggg ctcctgttgc a                                          21
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/872,185

DATE: 06/20/2001
TIME: 12:23:27

Input Set : A:\64080.txt
Output Set: N:\CRF3\06202001\I872185.raw

290 <210> SEQ ID NO: 14
291 <211> LENGTH: 21
292 <212> TYPE: DNA
293 <213> ORGANISM: Antisense Primer
295 <400> SEQUENCE: 14 21
296 ggccaaggct ggggttgaag g
299 <210> SEQ ID NO: 15
300 <211> LENGTH: 9
301 <212> TYPE: PRT
302 <213> ORGANISM: Peptide
304 <400> SEQUENCE: 15
306 Ala Ser Gln Arg Lys Pro Ser Gln Arg
307 1 5
309 <210> SEQ ID NO: 16
310 <211> LENGTH: 395
311 <212> TYPE: DNA
312 <213> ORGANISM: Bovine
314 <400> SEQUENCE: 16
315 atgactaagc tggaggacca cctggaggga atcatcaaca tcttccacca gtactccgtt 60
317 cggctgggac atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaaggga 120
319 gcttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180
321 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tggtgtccag 240
323 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttccagca atgttcccaa 300
325 gaagacttac ccttctcctc cctgaggctg ctccccgagg gagagagaat tataaacgta 360
327 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395

VERIFICATION SUMMARY DATE: 06/20/2001
PATENT APPLICATION: **US/09/872,185** TIME: 12:23:28

Input Set : **A:\64080.txt**
Output Set: **N:\CRF3\06202001\I872185.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9